Exiguobacterium indicum sp. nov., a psychrophilic bacterium from the Hamta glacier of the Himalayan mountain ranges of India

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Strain HHS 31^T, a Gram-positive, motile, rod-shaped, non-spore-forming, alkaliphilic bacterium, was isolated from the melt water of a glacier. Phenotypic and chemotaxonomic characteristics indicate that strain HHS 31^T is related to species of the genus *Exiguobacterium*. The 16S rRNA gene sequence similarities between HHS 31^T and strains of known species confirm that it is closely related to members of the genus *Exiguobacterium* (93–99 %) and that it exhibits > 97 % similarity with *Exiguobacterium acetylicum* DSM 20416^T (98.9 %), *Exiguobacterium antarcticum* DSM 14480^T (98.0 %), *Exiguobacterium oxidotolerans* JCM 12280^T (97.9 %) and *Exiguobacterium undae* DSM 14481^T (97.4 %). Phylogenetic analysis based on the 16S rRNA gene sequence further confirms the affiliation of HHS 31^T with the genus *Exiguobacterium*. However, the levels of DNA–DNA relatedness between HHS 31^T and *E. oxidotolerans* JCM 12280^T, *E. acetylicum* DSM 20416^T, *E. undae* DSM 14481^T and *E. antarcticum* DSM 14480^T are 50, 63, 67 and 28 %, respectively. Strain HHS 31^T also differs from these four closely related species in terms of a number of phenotypic traits. The phenotypic, chemotaxonomic and phylogenetic data suggest that HHS 31^T merits the status of a novel species, for which the name *Exiguobacterium indicum* sp. nov. is proposed. The type strain is HHS 31^T (=LMG 23471^T=IAM 15368^T).

The genus *Exiguobacterium* was created by Collins *et al.* (1983) to accommodate Gram-positive, non-spore-forming, facultatively anaerobic, alkaliphilic bacteria isolated from potato-processing effluent (Gee *et al.*, 1980). Since then, nine species have been described: *Exiguobacterium aurantiacum* (Collins *et al.*, 1983), *Exiguobacterium undae* and *Exiguobacterium antarcticum* (Fruhling *et al.*, 2002), *Exiguobacterium oxidotolerans* (Yumoto *et al.*, 2004), *Exiguobacterium aestuarii* and *Exiguobacterium marinum* (Kim *et al.*, 2005), *Exiguobacterium mexicanum* and *Exiguobacterium artemiae* (Lopez-Cortes *et al.*, 2006) and *Exiguobacterium acetylicum* (which was transferred from the genus *Brevibacterium*; Farrow *et al.*, 1994). In the present study, strain HHS 31^T was isolated from the melt water of the Hamta glacier located at a height of 4270 m above sea level in the Himalayan mountain ranges of India. The melt-water sample yielded about 2×10^4 c.f.u. ml⁻¹ and the pure colonies represented 26 different morphotypes (Shivaji *et al.*, 2005a). Representative strains from each morphotype were then tentatively identified, using their 16S rRNA gene

sequences (Shivaji *et al.*, 2005a), as being closely related to *Pseudomonas meridiana* (GenBank accession no. AJ537602), *Pseudomonas antarctica* (AJ537601), *Pseudomonas veronii* (AY267192), *Pseudomonas migulae* (AY047218), *Pseudomonas fluorescens* (AY538263), *Pseudomonas lini* (AY035996), *Pseudomonas jessinii* (AY391278), *Serratia marcescens* (AF076038), *Janthinobacterium lividum* (AY247410), *Bacillus subtilis* (AY672765), *Hafnia alvei* (AY572428), *E. acetylicum* (AY297792) and *Pedobacter cryoconitis* (AJ585231) (Shivaji *et al.*, 2005a). Two of the strains, HHS 11^T and HHS 22^T, were identified as representing novel species of *Dyadobacter* and *Pedobacter*, namely *Dyadobacter hamtensis* (Chaturvedi *et al.*, 2005) and *Pedobacter himalayensis* (Shivaji *et al.*, 2005a). In the present study, strain HHS 31^T, a Gram-positive, motile, non-spore-forming, rod-shaped bacterium, was identified, using polyphasic taxonomy, as representing a novel species of the genus *Exiguobacterium*.

Strain HHS 31^T was isolated by plating 1 ml glacial water on nutrient agar plates [0.5 % (w/v) peptone, 0.3 % (w/v) beef extract, 0.5 % (w/v) NaCl and 1.5 % (w/v) agar, pH 7.0] that were then incubated at 22 °C for 3 days. Nutrient agar medium was also used for maintaining strain HHS 31^T and for determining growth at various temperatures (5, 10, 15, 22, 28, 37 and 40 °C), at different pH values (pH 4, 6, 7, 8, 10 and 11) and in the presence of various concentrations of

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain HHS 31^T is AJ846291.

Strain HHS 31^T and various *Exiguobacterium* species are compared in a table of fatty acid compositions and a neighbour-joining phylogenetic tree available as supplementary material in IJSEM Online.

NaCl (5, 10, 12 and 15 %) (Shivaji *et al.*, 1989). The buffers used were MOPS (for pH 6.5–7.9) and CAPS (for pH 9.7–11.1). Phenotypic characteristics such as colony morphology, cell morphology, motility, various enzyme activities (as listed in Table 1) and sensitivity to antibiotics at 22 °C were ascertained using standard methods (Lanyi, 1987; Smibert & Krieg, 1994). Gas production was determined according to the method of Hugh & Leifson (1953). For acid production, the medium used was phenol red agar base (pH 7.4) containing proteose peptone (1 %), beef extract (0.1 %), NaCl (0.5 %), phenol red (0.0025 %) and agar (1.8 %). Minimal medium [K_2HPO_4 , 1.05 % (w/v); KH_2PO_4 , 0.45 % (w/v); $(NH_4)_2SO_4$, 0.1 % (w/v); agar, 1.5 % (w/v)] was used to evaluate the ability of the culture to assimilate various carbon compounds, including amino acids (0.5 %, w/v), when provided as the sole carbon source. Fatty acid methyl esters were prepared according to the method of Sato & Murata (1988) and analysed by GC (Shivaji *et al.*, 2004, 2005b, c). The G + C content of the DNA was determined by the spectrophotometric method (Shivaji *et al.*, 1989). Isoprenoid quinones were extracted according to the method described by Collins *et al.* (1977), separated by HPLC and identified as described by Reddy *et al.* (2003). Peptidoglycan was prepared and analysed according to the method described by Komagata & Suzuki (1987). DNA–DNA hybridization was performed by using the membrane filter method (Tourova & Antonov, 1987), as described previously (Shivaji *et al.*, 1992). *E. acetylicum* DSM 20416^T, *E. undae* DSM 14481^T, *E. antarcticum* DSM 14480^T and *E. oxidotolerans* JCM 12280^T were used as reference strains in studies relating to morphology, biochemical characteristics and the identification of fatty acids.

To establish the phylogenetic position of strain HHS 31^T, DNA was purified and the 16S rRNA gene was amplified and sequenced as described previously (Shivaji *et al.*, 2000). The almost-complete rRNA gene sequence (1503 bases) was manually aligned with those of closely related species by using CLUSTAL W (Thompson *et al.*, 1994) (see Supplementary Fig. S1 available in IJSEM Online) and phylogenetic affiliations were inferred using SEQBOOT, DNADIST and neighbour-joining from PHYLIP (Felsenstein, 1993). The Kimura two-parameter method was used for DNA distance calculations (Kimura, 1980), and bootstrap values were generated for 1000 replications of the data. In all cases, the input order of species added to the topology being constructed was randomized with the jumble option, with a random seed of 7 and 10 replications. Majority-rule (50 %) consensus trees were constructed (Page, 1996).

The phenotypic and chemotaxonomic characteristics of strain HHS 31^T are presented in the species description and in Table 1 (and in Supplementary Table S1 available in IJSEM Online). Strain HHS 31^T, which is Gram-positive, motile, rod-shaped, non-spore-forming, alkaliphilic, possesses MK-7 and MK-8 as the major menaquinones, has the Lys–Gly peptidoglycan type and has a DNA G + C content of

48 mol%, is similar to species of the genus *Exiguobacterium* (Collins *et al.*, 1983; Farrow *et al.*, 1994; Fruhling *et al.*, 2002; Yumoto *et al.*, 2004; Kim *et al.*, 2005; Lopez-Cortes *et al.*, 2006). Phylogenetic analysis based on the 16S rRNA gene sequence (1480 nt) and performed with the neighbour-joining algorithm further confirms the affiliation of HHS 31^T with the genus *Exiguobacterium*. All of the reported species of *Exiguobacterium* formed two distinct clusters, as reported previously (Lopez-Cortes *et al.*, 2006; Kim *et al.*, 2005). Strain HHS 31^T forms part of one of these clusters, which includes *E. acetylicum* DSM 20416^T, *E. oxidotolerans* JCM 12280^T, *E. undae* DSM 14481^T, *E. antarcticum* DSM 14480^T and *E. artemiae* DSM 16484^T (Supplementary Fig. S1). The coherence of the cluster is obvious from the high bootstrap value (> 78 %) between strains in the cluster. The remaining strains, namely *E. aurantiacum* NCDO 2321^T, *E. mexicanum* DSM 16483^T, *E. marinum* DSM 16307^T and *E. aestuarii* DSM 16306^T, form a separate clade.

Using GeneTool 1.0 (<http://www.biotoools.com>), the degrees of affiliation (i.e. 16S rRNA gene sequence similarity) between HHS 31^T and reported species of *Exiguobacterium* were 93.6 % (*E. aurantiacum* NCDO 2321^T; GenBank accession no. X70316), 94 % (*E. aestuarii* TF-16^T; AY594264), 94.2 % (*E. marinum* TF-80^T; AY594266), 94.2 % (*E. mexicanum* DSM 16483^T; AM072764), 96.2 % (*E. artemiae* DSM 16484^T; AM072763), 97.4 % (*E. undae* DSM 14481^T; AJ344151), 97.9 % (*E. oxidotolerans* T-2-2^T; AB105164), 98 % (*E. antarcticum* DSM 14480^T; AJ297437) and 98.9 % (*E. acetylicum* IFO 12146^T; D55730). Thus, strain HHS 31^T, which exhibits > 97 % 16S rRNA gene sequence similarity with the type strains of *E. acetylicum*, *E. antarcticum*, *E. oxidotolerans* and *E. undae*, needs to be differentiated from these four species to merit membership of a novel species. At the whole-genome level, as determined by DNA–DNA hybridization when strain HHS 31^T was radioactively labelled, the strain showed DNA–DNA hybridization values with *E. oxidotolerans* JCM 12280^T, *E. acetylicum* DSM 20416^T, *E. undae* DSM 14481^T and *E. antarcticum* DSM 14480^T of 50, 63, 67 and 28 %, respectively. However, when *E. oxidotolerans* JCM 12280^T, *E. acetylicum* DSM 20416^T and *E. undae* DSM 14481^T were labelled and used for DNA–DNA hybridization with HHS 31^T, the relatedness values were 49, 56 and 60 %, respectively. Furthermore, HHS 31^T differs from the closest species, *E. oxidotolerans*, *E. acetylicum*, *E. undae*, *E. antarcticum* and '*Exiguobacterium sibiricum*' (Rodrigues *et al.*, 2006), with respect to a number of phenotypic characteristics (Table 1) and also exhibits significant quantitative differences in fatty acid composition (Supplementary Table S1). The predominant fatty acids are iso-C_{15:0} (48.7 %) and iso-C_{17:0} (43 %), which together constituted ~ 92 % of the total fatty acid content. These two fatty acids were also predominant in the remaining five species of *Exiguobacterium* (Supplementary Table S1). However, an interesting feature is that the combined levels of iso-C_{15:0} (12–48.7 %) and iso-C_{17:0} (12–43 %) were highest in *E. indicum* HHS 31^T, *E. oxidotolerans* JCM

Table 1. Phenotypic characteristics that differentiate strain HHS 31^T and related type strains

Strains: 1, strain HHS 31^T; 2, *E. acetylicum* DSM 20416^T; 3, *E. oxidotolerans* JCM 12280^T; 4, *E. antarcticum* DSM 14480^T; 5, *E. undae* DSM 14481^T; 6, '*E. sibiricum*' DSM 17290. Data for all strains except '*E. sibiricum*' DSM 17290 (Rodrigues *et al.*, 2006) are from this study unless indicated. All of the strains shown are motile, Gram-positive, rod-shaped, do not form endospores, grow at temperatures between 10 and 30 °C (with optimum growth at 25 °C), tolerate up to 5·8% NaCl, grow in peptone, do not grow at pH 4, grow at pH 6–10, utilize dextrin and are positive for catalase, oxidase, β -galactosidase, arginine dihydrolase, ornithine decarboxylase and in the Voges–Proskauer test. All are negative for urease, H₂S production, in the indole test and for acid production from D-sorbitol, L-melibiose, D-lactose, L-arabinose and L-xylose. All utilize D-glucose, sucrose, glycerol and thioglycolate but do not utilize L-sorbose, D-arabinose, L-arabinose, D-lactose, D-adonitol, hydroxybutyric acid, dextran or sodium propionate. All are sensitive to the following antibiotics (μ g): tobramycin (15), lomefloxacin (30), roxithromycin (30), ciprofloxacin (30), lincomycin (15), cefotaxime (30), cefazolin (30), kanamycin (30), novobiocin (30), chloramphenicol (30), ampicillin (25), tetracycline (30), streptomycin (25), erythromycin (15), bacitracin (10), gentamicin G (30), polymyxin B (50), oleandomycin (15), spectinomycin (100), rifampicin (25) and carbenicillin (100). +, Positive; –, negative; ND, not done/no data available; +/-, variable reaction; W, weakly positive.

Characteristic	1	2	3	4	5	6
Habitat	Glacial water	Creamery waste	Drainage from fish-processing plant	Microbial mat from lake water	Garden pond	Permafrost
Colony morphology						
Size (mm)	2–4	2–5	1–5	2–3	2–4	3·5–4
Shape	Round	Irregular	Round	Round	Round	Round
Colour	Yellowish orange	Yellowish orange	Orange	Orange	Orange	Bright orange
Growth temperature (°C)						
2·5	W	–	W	–	–	+
5	+	–	+	–	–	+
37	–	W	+	+	+	+
Maximum growth temperature (°C)	30	37	40	41	41	40
Gelatinase	–	+	+	+	+	+
Lipase	–	–	–	–	–	+
Phosphatase	+	+	+	+	–	+
Aesculin hydrolysis	–	+	+	+	+	–
Starch hydrolysis	–	+	+	+	+	ND
Citrate utilization	+	+	+	–	–	ND
Lysine decarboxylase	+	–	–	–	+	ND
Arginine decarboxylase	+	–	–	+	+	ND
DNase, caseinase	–	+	+	+	+	ND
Tryptophan deamination	–	+	+	+	–	ND
Reduction of NO ₃ [–] to NO ₂ [–]	+	–	–	–	–	–
Methyl red test	–	+	+	+	+	ND
Malonate utilization	+	–	–	–	–	ND
Acid production from:						
Inulin	–	–	–	–	–	ND
D-Glucose, sucrose, D-fructose, D-trehalose, maltose, L-rhamnose, D-ribose	–	+	+	+	+	ND
D-Mannose	–	+	+	–	+	ND
D-Cellobiose	–	+	–	+	–	ND
D-Adonitol	–	+	–	–	–	ND
Carbon-source utilization						
D-Galactose	+	–	–	–	+	+
L-Rhamnose, L-melibiose, D-xylose	+	–	–	–	–	+/-
D-Cellobiose	+	+	–	+	+	+
D-Fructose, D-mannose, D-trehalose, D-ribose, maltose	–	+	+	+	+	+

Table 1. cont.

Characteristic	1	2	3	4	5	6
L-Xylose	+	—	—	—	—	ND
D-Mannitol	—	+	+	—	+	+
D-Raffinose	+	—	—	+	+	+
Lactic acid, D-sorbitol, dulcitol	+	—	—	—	—	—
Fumaric acid	+	—	—	—	—	ND
D-Melezitose	—	+	—	—	—	+ / —
Polyethylene glycol	+	—	—	—	+	ND
N-Acetylglucosamine	—	—	—	—	—	+
Citric acid, sodium acetate	+	—	—	+	+	ND
Potassium acetate	+	—	—	—	+	ND
Cellulose	—	—	—	—	+	ND
Starch	—	+	+	+	+	+
Inulin, <i>myo</i> -inositol	+	—	—	—	—	—
Pyruvate	—	+	+	+	+	+
Glycogen	+	—	—	+	+	ND
Methyl α -D-mannoside	—	+	—	+	—	—
Methyl α -D-glucoside	—	+	+	—	+	—
Methyl α -D-galactoside	+	—	—	—	—	—
Methyl β -D-galactoside	+	—	—	—	—	+
Arbutin	+	—	+	+	+	+
Salicin	—	+	—	—	+	+
Amygdalin	—	—	+	+	+	+
Xylitol, L-fucose	—	+	—	—	—	—
L-Malic acid	+	—	—	—	—	+ / —
Erythritol	+	—	+	—	+	ND
Sodium gluconate, 5-ketogluconate	+	—	—	—	—	—
Sodium fumarate, sodium formate	+	—	—	+	—	ND
Sodium succinate	+	—	—	—	+	+
γ -Glucuronic acid	+	—	—	—	+	ND
α -Ketoglutaric acid	+	—	—	—	+	—
Valeric acid	+	—	—	+	—	+
Amino acids used						
L-Glycine	+	—	—	—	+	ND
L-Ornithine, L-valine, L-threonine, L-arginine, L-proline, L-histidine	+	—	—	+	+	ND
L-Alanine	+	—	—	+	+	—
L-Leucine, L-tyrosine	+	+	—	+	+	ND
L-Isoleucine, L-lysine, L-glutamine, L-methionine	+	—	+	+	+	ND
L-Serine	+	—	+	—	+	+ / —
L-Glutamic acid	+	—	—	+	—	+ / —
L-Aspartic acid	+	—	+	—	+	ND
L-Asparagine	+	—	—	+	+	+
L-Cysteine	—	—	—	+	+	ND
L-Phenylalanine	—	—	—	—	—	ND
L-Tryptophan	+	—	—	+	—	ND
L-Creatinine	+	—	—	—	—	ND
Antibiotic tolerance (μ g per disc)*						
Norfloxacin (10)	R	S	S	S	S	ND
Amikacin (30)	R	S	S	S	S	ND
Nitrofurantoin (300)	R	S	S	S	S	ND
Cotrimoxazole (25)	R	S	S	S	S	ND
Amoxycillin (30)	R	S	S	S	S	ND
Nalidixic acid (30)	R	S	S	S	S	ND

Table 1. cont.

Characteristic	1	2	3	4	5	6
Sulfamethoxazole (50)	R	S	S	S	R	ND
Doxycycline (25)	R	S	S	S	S	ND
Clindamycin (25)	R	R	S	S	S	ND
Colistin (10)	R	S	R	R	S	ND
DNA G + C content (mol%)	48	47	47	47	48	47.7
Peptidoglycan†	Lys–Gly	Lys–Gly	Lys–Gly	ND	Lys–Asp	Lys–Gly
Quinone(s)	MK-7, MK-8	MK-7	MK-6, MK-7, MK-8	MK-6, MK-7, MK-8	MK-6, MK-7, MK-8	MK-6, MK-7, MK-8
Polar lipids‡	PG, DPG, PE (traces)	DPG, PS	PG, DPG, PE, PS, PI, unidentified	PG, DPG, PE, PS, PI, unidentified	PG, DPG, PE, PS, PI, unidentified	PG, DPG, PE

*R, Resistant; S, sensitive.

†Determined for HHS 31^T, *E. acetylicum* DSM 20416^T and *E. undae* DSM 14481^T in this study. Peptidoglycan compositions for *E. oxidotolerans* JCM 12280^T, *E. antarcticum* DSM 14480^T and '*E. sibiricum*' DSM 17290 were taken from Yumoto *et al.* (2004), Fruhling *et al.* (2002) and Rodrigues *et al.* (2006), respectively.

‡DPG, Diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PI, phosphatidylinositol; PS, phosphatidylserine.

12280^T and '*E. sibiricum*' DSM 17290. These three species grow at 2.5 °C, unlike the other species. Thus, these fatty acids (iso-C_{15:0} and iso-C_{17:0}) may be required for growth at low temperatures. According to the criteria for species discrimination (Stackebrandt & Goebel, 1994), strain HHS 31^T, which exhibits <70 % relatedness at the DNA–DNA level with the type strains of *E. oxidotolerans*, *E. antarcticum*, *E. acetylicum* and *E. undae* (the most closely related species) and which also differs phenotypically from these four species, represents a novel species of the genus *Exiguobacterium*, for which the name *Exiguobacterium indicum* sp. nov. is proposed.

Description of *Exiguobacterium indicum* sp. nov.

Exiguobacterium indicum (in 'di.cum. L. neut. adj. *indicum* Indian, pertaining to India).

Cells are aerobic, Gram-positive, motile and rod-shaped (2.3 µm long and 0.52 µm wide). Stationary-phase cells are coccobacilli. Colonies (2–4 mm) on nutrient agar are round, shiny, irregular, elevated and orange-coloured after 24 h at 22 °C. No spores are observed. Grows at 5–30 °C and at pH 6–10. The optimum temperature and pH for growth are 25 °C and pH 7.0. Tolerates 5.8 % NaCl and also grows in the absence of salt. Colonies are yellowish orange in colour. The pigment is soluble in chloroform and exhibits multiple absorption maxima at 408, 434, 460 and 495 nm. Positive for catalase, oxidase, β-galactosidase, phosphatase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, arginine decarboxylase, citrate utilization, malonate utilization, in the Voges–Proskauer test and for reduction of nitrate to nitrite. Negative for urease, lipase, gelatinase, DNase, caseinase, tryptophan deamination, indole production, in the methyl red test, for H₂S production and for hydrolysis of aesculin and starch hydrolysis. Utilizes D-glucose, D-galactose, D-rhamnose,

L-melibiose, D-cellobiose, sucrose, D-xylose, L-xylose, D-raffinose, glycerol, lactic acid, fumaric acid, N-acetylglucosamine, D-sorbitol, dulcitol, polyethylene glycol, citric acid, sodium acetate, potassium acetate, inulin, dextrin, myo-inositol, glycogen, sodium thioglycolate, methyl α-D-galactoside, methyl β-D-galactoside, arbutin, malic acid, erythritol, sodium gluconate, sodium fumarate, sodium formate, sodium succinate, γ-glucuronic acid, α-ketoglutaric acid, valeric acid, 5-ketogluconate, L-glycine, L-ornithine, L-alanine, L-valine, L-leucine, L-isoleucine, L-serine, L-threonine, L-lysine, L-arginine, L-glutamic acid, L-aspartic acid, glutamine, L-asparagine, L-methionine, L-tyrosine, L-tryptophan, L-proline, L-histidine and L-creatinine, but not L-sorbose, L- or D-arabinose, D-fructose, D-mannose, D-trehalose, D-mannitol, D-ribose, D-lactose, D-adonitol, maltose, D-melezitose, hydroxybutyric acid, dextran, sodium propionate, cellulose, starch, pyruvate, methyl α-D-mannoside, methyl α-D-glucoside, salicin, amygdalin, xylitol, L-fucose, L-cysteine or L-phenylalanine. Negative for acid production from inulin, D-glucose, sucrose, D-fructose, D-sorbitol, L-melibiose, D-lactose, D-trehalose, maltose, L-rhamnose, D-mannose, L-arabinose, L-xylose, D-ribose, D-cellobiose and adonitol. Resistant to discs containing the following antibiotics (µg): norfloxacin (10), cotrimoxazole (25), clindamycin (25), doxycycline (25), sulfamethoxazole (50), amoxicillin (30), amikacin (30), nalidixic acid (30), nitrofurantoin (300) and colistin (10). Sensitive to the following antibiotics (µg): tobramycin (15), lomefloxacin (30), roxithromycin (30), ciprofloxacin (30), penicillin (10), cefoperazone (75), vancomycin (30), cefuroxime (30), lincomycin (15), cefotaxime (30), cefazolin (30), kanamycin (30), novobiocin (30), chloramphenicol (30), ampicillin (25), tetracycline (30), streptomycin (25), erythromycin (15), bacitracin (10), gentamicin G (30), polymyxin B (50), oleandomycin (15), spectinomycin (100), rifampicin (25) and carbenicillin (100). Major respiratory

quinones are MK-7 and MK-8. Peptidoglycan is of the Lys-Gly type. Phosphatidylglycerol and diphosphatidylglycerol are the main phospholipids; minute amounts of phosphatidylethanolamine are also present. The DNA G + C content is 48.0 mol%. The fatty acids present are iso-C_{13:0} (0.2 %), iso-C_{15:0} (48.7 %), iso-C_{16:0} (3.0 %), C_{16:1} (0.3 %), iso-C_{17:0} (43.0 %), anteiso-C_{17:0} (0.3 %) and C_{18:1} (2.0 %).

The type strain, HHS 31^T (=LMG 23471^T =IAM 15368^T), was isolated from melt water from the Hamta glacier located at a height of 4279 m above sea level in the Himalayan mountain ranges of India.

Acknowledgements

We thank the Department of Biotechnology of the Government of India (New Delhi, India) for a research grant awarded to S.S. We are grateful to Dr Jean Euzéby for helping us with the naming of the novel species.

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